WHAT IS CLAIMED IS:

1. A detection probe for use determining the presence of SARS-CoV in a test sample, said probe being up to 100 bases in length and comprising a target binding portion which forms a hybrid stable for detection with a target sequence contained within the sequence of SEQ ID NO:1 or its complement under stringent hybridization conditions, wherein said probe does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said conditions.

2. The probe of claim 1, wherein said target binding portion comprises an at least 10 contiguous base region which is perfectly complementary to an at least 10 contiguous base region of said target sequence or its complement.

3. The probe of claim 1, wherein said target binding portion comprises an at least 15 contiguous base region which is perfectly complementary to an at least 15 contiguous base region of said target sequence or its complement.

4. The probe of claim 1, wherein said probe comprises a base sequence selected from the group consisting of SEQ ID NO:2, its complement, and the RNA equivalents thereof.

5. The probe of claim 1, wherein the base sequence of said probe consists of a base sequence selected from the group consisting of SEQ ID NO:2, its complement, and the RNA equivalents thereof.

6. The probe of claim 1, wherein the base sequence of said target binding portion is perfectly complementary to all or a portion of the base sequence of SEQ ID NO:1 or its complement, and wherein said probe does not comprise any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said conditions.

7. The probe of claim 6, wherein said target binding portion comprises an at least 10 contiguous base region which is perfectly complementary to an at least 10 contiguous base region of SEQ ID NO:1 or its complement.

8. The probe of claim 6, wherein said target binding portion comprises an at least 15 contiguous base region which is perfectly complementary to an at least 15 contiguous base region of SEQ ID NO:1 or its complement.

9. The probe of claim 6, wherein said probe is a self-hybridizing probe under said conditions and in the absence of said target sequence.

10. The probe of claim 9, wherein said probe comprises a pair of interacting labels.

11. The probe of claim 10, wherein said pair of interacting labels is selected from the group consisting of a luminescent/quencher pair, a luminescent/adduct pair, a Förrester energy transfer pair and a dye dimer.

12. The probe of claim 1, wherein said probe comprises a detectable label.

13. The probe of claim 1, wherein said conditions include a temperature of about 60°C and a salt concentration of about 0.6 M to about 0.9 M.

14. A method for determining the presence of SARS-CoV in a test sample, said method comprising the steps of:

a) contacting a test sample with said probe of claim 1 under said conditions; and

b) determining whether said hybrid is present in said test sample as an indication of the presence of SARS-CoV in said test sample.

15. A detection probe for use determining the presence of SARS-CoV in a test sample, said probe being up to 100 bases in length and comprising a target binding portion which forms a hybrid stable for detection with a target sequence contained within the sequence of SEQ ID NO:3 or its complement under stringent hybridization conditions, wherein said probe does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said conditions.

16. The probe of claim 15, wherein said target binding portion comprises an at least 10 contiguous base region which is perfectly complementary to an at least 10 contiguous base region of said target sequence or its complement.

17. The probe of claim 15, wherein said target binding portion comprises an at least 15 contiguous base region which is perfectly complementary to an at least 15 contiguous base region of said target sequence or its complement.

18. The probe of claim 15, wherein the base sequence of said target binding portion is perfectly complementary to all or a portion of the base sequence of SEQ ID NO:3 or its complement, and wherein said probe does not comprise any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said conditions.

19. The probe of claim 18, wherein said target binding portion comprises an at least 10 contiguous base region which is perfectly complementary to an at least 10 contiguous base region of SEQ ID NO:3 or its complement.

20. The probe of claim 18, wherein said target binding portion comprises an at least 15 contiguous base region which is perfectly complementary to an at least 15 contiguous base region of SEQ ID NO:3 or its complement.

21. The probe of claim 15, wherein said probe comprises a base sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5 and SEQ ID NO:6, their complements, and the RNA equivalents thereof.

22. The probe of claim 15, wherein the base sequence of said target binding portion is contained within a base sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5 and SEQ ID NO:6, their complements, and the RNA equivalents thereof, and wherein said probe does not comprise any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said conditions.

23. The probe of claim 22, wherein the base sequence of said target binding portion is contained within a base sequence selected from the group consisting of SEQ ID NO:4, its complement, and the RNA equivalents thereof.

24. The probe of claim 23, wherein the base sequence of said target binding portion consists of a base sequence selected from the group consisting of SEQ ID NO:4, its complement, and the RNA equivalents thereof.

25. The probe of claim 24, wherein the base sequence of said probe consists of a base sequence selected from the group consisting of SEQ ID NO:4, its complement, and the RNA equivalents thereof.

26. The probe of claim 22, wherein the base sequence of said target binding portion is contained within a base sequence selected from the group consisting of SEQ ID NO:5, its complement, and the RNA equivalents thereof.

27. The probe of claim 26, wherein the base sequence of said target binding portion consists of a base sequence selected from the group consisting of SEQ ID NO:5, its complement, and the RNA equivalents thereof.

28. The probe of claim 27, wherein the base sequence of said probe consists of a base sequence selected from the group consisting of SEQ ID NO:5, its complement, and the RNA equivalents thereof.

29. The probe of claim 22, wherein the base sequence of said target binding portion is contained within a base sequence selected from the group consisting of SEQ ID NO:6, its complement, and the RNA equivalents thereof.

30. The probe of claim 29, wherein the base sequence of said target binding portion consists of a base sequence selected from the group consisting of SEQ ID NO:6, its complement, and the RNA equivalents thereof.

31. The probe of claim 30, wherein the base sequence of said probe consists of a base sequence selected from the group consisting of SEQ ID NO:6, its complement, and the RNA equivalents thereof.

32. The probe of claim 18, wherein said probe is a self-hybridizing probe under said conditions and in the absence of said target sequence.

33. The probe of claim 32, wherein said probe comprises a pair of interacting labels.

34. The probe of claim 33, wherein said pair of interacting labels is selected from the group consisting of a luminescent/quencher pair, a luminescent/adduct pair, a Förrester energy transfer pair and a dye dimer.

35. The probe of claim 15, wherein said probe comprises a detectable label.

36. The probe of claim 15, wherein said conditions include a temperature of about 60°C and a salt concentration of about 0.6 M to about 0.9 M.

37. A method for determining the presence of SARS-CoV in a test sample, said method comprising the steps of:

a) contacting a test sample with said probe of claim 16 under said conditions; and

b) determining whether said hybrid is present in said test sample as indication of the presence of SARS-CoV in said test sample.

38. An oligonucleotide set comprising two or more oligonucleotides capable of amplifying a target region of nucleic acid derived from SARS-CoV under amplification conditions, said target region being contained within the sequence of SEQ ID NO:8 or its complement.

39. The oligonucleotide set of claim 38, wherein said set comprises:

a first oligonucleotide up to 100 bases in length which binds to or extends through a first target sequence contained within the sequence of SEQ ID NO:9 or its complement under amplification conditions; and

a second oligonucleotide up to 100 bases in length which binds to or extends through a second target sequence contained within the sequence of SEQ ID NO:10 or its complement under amplification conditions.

40. The oligonucleotide set of claim 39, wherein said first target sequence is selected from the group consisting of SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18 and SEQ ID NO:19, and their complements.

41. The oligonucleotide set of claim 39, wherein said second target sequence is selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22, and their complements.

42. The oligonucleotide set of claim 40, wherein said second target sequence is selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22, and their complements.

43. The oligonucleotide set of claim 39, wherein said first oligonucleotide comprises a base sequence selected from the group consisting of SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18 and SEQ ID NO:19, their complements, and the DNA equivalents thereof.

44. The oligonucleotide set of claim 39, wherein said second oligonucleotide comprises a base sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22, their complements, and the DNA equivalents thereof.

45. The oligonucleotide set of claim 43, wherein said second oligonucleotide comprises a base sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22, their complements, and the DNA equivalents thereof.

46. The oligonucleotide set of claim 39, wherein the base sequence of said first oligonucleotide is contained within a base sequence selected from the group consisting of SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18 and SEQ ID NO:19, their complements, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by RNA polymerase.

47. The oligonucleotide set of claim 39, wherein the base sequence of said second oligonucleotide is contained within a base sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22, their complements, the DNA

equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by RNA polymerase.

48. The oligonucleotide set of claim 46, wherein the base sequence of said second oligonucleotide is contained within a base sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22, their complements, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by RNA polymerase.

49. The oligonucleotide set of claim 39, wherein the base sequence of said first oligonucleotide consists of a base sequence selected from the group consisting of SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18 and SEQ ID NO:19, their complements, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by RNA polymerase.

50. The oligonucleotide set of claim 39, wherein the base sequence of said second oligonucleotide consists of a base sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22, their complements, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by RNA polymerase.

51. The oligonucleotide set of claim 49, wherein the base sequence of said second oligonucleotide consists of a base sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22, their complements, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by RNA polymerase.

52. The oligonucleotide set of claim 51, wherein at least one of said first and second oligonucleotides comprises a T7 promoter sequence.

53. The oligonucleotide set of claim 38 further comprising a third oligonucleotide for use in determining the presence of a target sequence derived from said target region of SARS-CoV-derived nucleic acid, said third oligonucleotide being up to 100 bases in length and comprising a target binding portion which forms a hybrid stable for detection with said target sequence under stringent hybridization conditions, wherein said third oligonucleotide does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said stringent hybridization conditions.

54. The oligonucleotide set of claim 53, wherein said target binding portion is complementary to the sequence of SEQ ID NO:1 or its complement.

55. The oligonucleotide set of claim 54, wherein the base sequence of said target binding portion is contained within a base sequence selected from the group consisting of SEQ ID NO:1, its complement, and the DNA equivalents thereof, and wherein said third oligonucleotide does not comprise any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said stringent hybridization conditions.

56. The oligonucleotide set of claim 55, wherein said third oligonucleotide is a self-hybridizing oligonucleotide under said stringent hybridization conditions and in the absence of said target sequence.

57. The oligonucleotide of claim 56, wherein said third oligonucleotide comprises a pair of interacting labels.

58. The oligonucleotide set of claim 53, wherein the base sequence of said third oligonucleotide consists of a base sequence selected from the group consisting of SEQ ID NO:2, its complement, and the RNA equivalents thereof.

59. The oligonucleotide set of claim 53, wherein said third oligonucleotide comprises a detectable label.

60. The oligonucleotide set of claim 38 further comprising a third oligonucleotide for use in isolating and purifying a target nucleic acid containing said target region of SARS-CoV-derived nucleic acid, said third oligonucleotide being up to 100 bases in length and comprising a target binding portion that is complementary to a target sequence selected from the group consisting of SEQ ID NO:35, SEQ ID NO:36 and SEQ ID NO:37, wherein said third oligonucleotide stably hybridizes to said target sequence under assay conditions.

61. The oligonucleotide set of claim 60, wherein the base sequence of said target binding portion of said third oligonucleotide is contained within a base sequence selected from the group consisting of the complements of SEQ ID NO:35, SEQ ID NO:36 and SEQ ID NO:37, and the DNA equivalents thereof, and wherein said third oligonucleotide does not comprise any other base sequences which stably hybridize to SARS-CoV-derived nucleic acid under said assay conditions.

62. The oligonucleotide set of claim 61, wherein the base sequence of said target binding portion of said third oligonucleotide consists of a base sequence selected from the group consisting of the complements of SEQ ID NO:35, SEQ ID NO:36 and SEQ ID NO:37, and the DNA equivalents thereof.

63. The oligonucleotide set of claim 53 further comprising a fourth oligonucleotide for use in isolating and purifying a target nucleic acid containing said target region of SARS-CoV-derived nucleic acid, said fourth oligonucleotide being up to 100 bases in length and comprising a target binding portion that is complementary to a target sequence selected from the group consisting of SEQ ID NO:35, SEQ ID NO:36 and SEQ ID NO:37, wherein said fourth oligonucleotide stably hybridizes to said target sequence under assay conditions.

64. A method for amplifying a target region of nucleic acid derived from SARS-CoV, said method comprising the steps of:

a) contacting a test sample with said two or more oligonucleotides of claim 38; and

b) exposing said test sample to said amplification conditions such that said target region, if present in said test sample, is amplified.

65. A method for determining the presence of SARS-CoV in a test sample, said method comprising the steps of:

a) contacting a test sample with said first and second oligonucleotides of claim 39 under said amplification conditions;

b) amplifying, if present in said test sample, said target region;

c) contacting said test sample a third oligonucleotide, said third oligonucleotide being up to 100 bases in length and comprising a target binding portion which forms a hybrid stable for detection with a sequence contained within or complementary to said target region under stringent hybridization conditions, wherein said third oligonucleotide does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said stringent hybridization conditions; and

d) determining whether said hybrid is present in said test sample as indication of the presence of SARS-CoV in said test sample.

66. The method of claim 65, wherein said third oligonucleotide is provided to said test sample prior to or during said amplifying step.

67. The method of claim 66, wherein at least a portion of said determining step occurs during said amplifying step.

68. An oligonucleotide set comprising two or more oligonucleotides capable of amplifying a target region of nucleic acid derived from SARS-CoV under amplification conditions, said target region being contained within the sequence of SEQ ID NO:23 or its complement.

69. The oligonucleotide set of claim 68, wherein said set comprises:

a first oligonucleotide up to 100 bases in length which binds to or extends through a first target sequence contained within the sequence of SEQ ID NO:24 or its complement under amplification conditions; and

a second oligonucleotide up to 100 bases in length which binds to or extends through a second target sequence contained within the sequence of SEQ ID NO:25 or its complement under amplification conditions.

70. The oligonucleotide set of claim 69, wherein said first target sequence is selected from the group consisting of SEQ ID NO:26 and SEQ ID NO:27, and their complements.

71. The oligonucleotide set of claim 69, wherein said second target sequence is selected from the group consisting of SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32 and SEQ ID NO:33, and their complements.

72. The oligonucleotide set of claim 70, wherein said second target sequence is selected from the group consisting of SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32 and SEQ ID NO:33, and their complements.

73. The oligonucleotide set of claim 69, wherein said first oligonucleotide comprises a base sequence selected from the group consisting of SEQ ID NO:26 and SEQ ID NO:27, their complements, and the DNA equivalents thereof.

74. The oligonucleotide set of claim 69, wherein said second oligonucleotide comprises a base sequence selected from the group consisting of SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32 and SEQ ID NO:33, their complements, and the DNA equivalents thereof.

75. The oligonucleotide set of claim 73, wherein said second oligonucleotide comprises a base sequence selected from the group consisting of SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32 and SEQ ID NO:33, their complements, and the DNA equivalents thereof.

76. The oligonucleotide set of claim 69, wherein the base sequence of said first oligonucleotide is contained within a base sequence selected from the group consisting of SEQ ID NO:26 and SEQ ID NO:27, their complements, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by RNA polymerase.

77. The oligonucleotide set of claim 69, wherein the base sequence of said second oligonucleotide is contained within a base sequence selected from the group consisting of SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32 and SEQ ID NO:33, their complements, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by RNA polymerase.

78. The oligonucleotide set of claim 76, wherein the base sequence of said second oligonucleotide is contained within a base sequence selected from the group consisting of SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32 and SEQ ID NO:33, their complements, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by RNA polymerase.

79. The oligonucleotide set of claim 69, wherein the base sequence of said first oligonucleotide consists of a base sequence selected from the group consisting of SEQ ID NO:26 and SEQ ID NO:27, their complements, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by RNA polymerase.

80. The oligonucleotide set of claim 69, wherein the base sequence of said second oligonucleotide consists of a base sequence selected from the group consisting of SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32 and SEQ ID NO:33, their complements, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by RNA polymerase.

81. The oligonucleotide set of claim 79, wherein the base sequence of said second oligonucleotide consists of a base sequence selected from the group consisting of SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32 and SEQ ID NO:33, their complements, the DNA equivalents thereof, and any of the foregoing in combination with a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by RNA polymerase.

82. The oligonucleotide set of claim 81, wherein at least one of said first and second oligonucleotides comprises a T7 promoter sequence.

83. The oligonucleotide set of claim 68 further comprising a third oligonucleotide for use in determining the presence of a target sequence derived from said target region of SARS-CoV-derived nucleic acid, said third oligonucleotide being up to 100 bases in length and comprising a target binding portion which forms a hybrid stable for detection with said target sequence under stringent hybridization conditions, wherein said third oligonucleotide does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said stringent hybridization conditions.

84. The oligonucleotide set of claim 83, wherein said target binding portion is complementary to the sequence of SEQ ID NO:3 or its complement.

85. The oligonucleotide set of claim 83, wherein the base sequence of said target binding portion is contained within a base sequence selected from the group consisting of SEQ ID NO:3, its complement, and the DNA equivalents thereof, and wherein said third oligonucleotide does not comprise any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said stringent hybridization conditions.

86. The oligonucleotide set of claim 85, wherein the base sequence of said target binding portion is contained within a base sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5 and SEQ ID NO:6, their complements, and the RNA equivalents thereof, and wherein said third oligonucleotide does not comprise any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said stringent hybridization conditions.

87. The oligonucleotide set of claim 86, wherein said third oligonucleotide is a self-hybridizing oligonucleotide under said stringent hybridization conditions and in the absence of said target sequence.

88. The oligonucleotide of claim 87, wherein said third oligonucleotide comprises a pair of interacting labels.

89. The oligonucleotide set of claim 83, wherein the base sequence of said third oligonucleotide consists of a base sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:5 and SEQ ID NO:6, their complements, and the RNA equivalents thereof.

90. The oligonucleotide set of claim 83, wherein said third oligonucleotide comprises a detectable label.

91. The oligonucleotide set of claim 68 further comprising a third oligonucleotide for use in isolating and purifying a target nucleic acid containing said target region of SARS-CoV-derived nucleic acid, said third oligonucleotide being up to 100 bases in length and comprising a target binding portion that is complementary to a target sequence selected from the group consisting of SEQ ID NO:35, SEQ ID NO:36 and SEQ ID NO:37, and wherein said third oligonucleotide stably hybridizes to said target sequence under assay conditions.

92. The oligonucleotide set of claim 91, wherein the base sequence of said target binding portion of said third oligonucleotide is contained within a base sequence selected from the group consisting of the complements of SEQ ID NO:35, SEQ ID NO:36 and SEQ ID NO:37, and the DNA equivalents thereof, and wherein said third oligonucleotide does not comprise any other base sequences which stably hybridize to SARS-CoV-derived nucleic acid under said assay conditions.

93. The oligonucleotide set of claim 92, wherein the base sequence of said target binding portion of said third oligonucleotide consists of a base sequence selected from the group consisting of the complements of SEQ ID NO:35, SEQ ID NO:36 and SEQ ID NO:37 and the DNA equivalents thereof.

94. The oligonucleotide set of claim 83 further comprising a fourth oligonucleotide for use in isolating and purifying a target nucleic acid containing said target region of SARS-CoV-derived nucleic acid, said fourth oligonucleotide being up to 100 bases in length and comprising a target binding portion that is complementary to a target sequence selected from the group consisting of SEQ ID NO:35, SEQ ID NO:36 and SEQ ID NO:37, and wherein said fourth oligonucleotide stably hybridizes to said target sequence under assay conditions.

95. A method for amplifying a target region of nucleic acid derived from SARS-CoV, said method comprising the steps of:

a) contacting a test sample with said two or more oligonucleotides of claim 68; and

b) exposing said test sample to said amplification conditions such that said target region, if present in said test sample, is amplified.

96. A method for determining the presence of SARS-CoV in a test sample, said method comprising the steps of:

a) contacting a test sample with said first and second oligonucleotides of claim 69 under said amplification conditions;

b) amplifying, if present in said test sample, said target region;

c) contacting to said test sample a third oligonucleotide, said third oligonucleotide being up to 100 bases in length and comprising a target binding portion which forms a hybrid stable for detection with a sequence contained within or complementary to said target region under stringent hybridization conditions, wherein said third oligonucleotide does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said stringent hybridization conditions; and

d) determining whether said hybrid is present in said test sample as indication of the presence of SARS-CoV in said test sample.

97. The method of claim 96, wherein said third oligonucleotide is provided to said test sample prior to or during said amplifying step.

98. The method of claim 97, wherein at least a portion of said determining step occurs during said amplifying step.

99. A method for determining the presence of SARS-CoV in a test sample, said method comprising the steps of:

a) contacting a test sample a detection probe up to 100 bases in length and comprising a target binding portion which forms a hybrid stable for detection with a target sequence contained within a SARS-CoV 5' leader sequence or its complement, wherein said

probe does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said conditions; and

b) determining whether said hybrid is present in said test sample as an indication of the presence of SARS-CoV in said test sample.

100. The method of claim 99, wherein said target sequence comprises a core sequence of a transcription regulating sequence or its complement.

101. The method of claim 100, wherein said core sequence consists of at least 5 contiguous nucleotides of the sequence of SEQ ID NO:38 or its complement.

102. The method of claim 101, wherein the core sequence consists of the sequence of SEQ ID NO:38 or its complement.

103. The method of claim 99 further comprising contacting said test sample with a pair of amplification oligonucleotides under amplification conditions, wherein each member of said pair of amplification oligonucleotides comprises a target binding portion which binds to or extends through at least a portion of said 5' leader sequence or its complement under said amplification conditions.

104. The method of claim 103, wherein said target binding portion of each member of said pair of amplification oligonucleotides binds to a target region fully contained within said 5' leader sequence or its complement under said amplification conditions, and wherein said amplification oligonucleotides do not contain any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said amplification conditions.

105. The method of claim 99 further comprising contacting said test sample with a pair of amplification oligonucleotides under amplification conditions, wherein a target binding portion of a first member of said pair of amplification oligonucleotides binds to a target region fully contained within said 5' leader sequence or its complement under said

amplification conditions, and wherein a target binding portion of a second member of said pair of amplification oligonucleotides binds to a target region fully contained within a SARS-CoV 3' co-terminal sequence or its complement under said amplification conditions, wherein said amplification oligonucleotides do not contain any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said amplification conditions.

106. A method for amplifying a target region of nucleic acid derived from SARS-CoV, said method comprising the steps of:

a) contacting a test sample with one or more amplification oligonucleotides under amplification conditions, wherein a first of said amplification oligonucleotides comprises a target binding portion which binds to a target region fully contained within a SARS-CoV 5' leader sequence or its complement under said conditions, wherein said first amplification oligonucleotide does not contain any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said amplification conditions; and

b) exposing said test sample to said conditions such that said target region, if present in said test sample, is amplified.

107. The method of claim 106, wherein said target region comprises a core sequence of a transcription regulating sequence or its complement.

108. The method of claim 107, wherein said core sequence consists of at least 5 contiguous nucleotides of the sequence of SEQ ID NO:38 or its complement.

109. The method of claim 108, wherein the core sequence consists of the sequence of SEQ ID NO:38 or its complement.

110. The method of claim 106, wherein said test sample is contacted with a pair of said amplification oligonucleotides under said conditions, wherein a second of said amplification oligonucleotides comprises a target binding portion which binds to a target

region fully contained within said 5' leader sequence or its complement under said conditions, and wherein said second amplification oligonucleotide does not contain any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said conditions.

111. A method for determining the presence of SARS-CoV in a test sample, said method comprising the steps of:

a) contacting a test sample with a detection probe up to 100 bases in length and comprising a target binding portion which forms a hybrid stable for detection with a target sequence contained within a SARS-CoV 3' co-terminal sequence or its complement, wherein said probe forms a hybrid stable for detection with said target sequence under stringent hybridization conditions, and wherein said probe does not form a hybrid stable for detection with nucleic acid derived from HCoV-OC43 or HCoV-229E under said conditions; and

b) determining whether said hybrid is present in said test sample as an indication of the presence of SARS-CoV in said test sample.

112. The method of claim 111 further comprising contacting said test sample with a pair of amplification oligonucleotides under amplification conditions, wherein each member of said pair of amplification oligonucleotides comprises a target binding portion which binds or extends through at least a portion of said 3' co-terminal sequence or its complement under said amplification conditions.

113. The method of claim 111, wherein said target binding portion of each member of said pair of amplification oligonucleotides binds to a target region fully contained within said 3' co-terminal sequence or its complement under said amplification conditions, and wherein said amplification oligonucleotides do not contain any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said amplification conditions.

114. A method for amplifying a target region of nucleic acid derived from SARS-CoV, said method comprising the steps of:

a) contacting a test sample with one or more amplification oligonucleotides under amplification conditions, wherein a first of said amplification oligonucleotides comprises a target binding portion which binds to a target region contained within a SARS-CoV 3' co-terminal sequence or its complement under said conditions; and

b) exposing said test sample to said conditions such that said target region, if present in said test sample, is amplified.

115. The method of claim 114, wherein said test sample is contacted with a pair of said amplification oligonucleotides under said conditions, wherein a second of said amplification oligonucleotides comprises a target binding portion which binds to a target region fully contained within said 3' co-terminal sequence or its complement under said conditions, and wherein said second amplification oligonucleotide does not contain any other base sequences which stably hybridize to nucleic acid derived from SARS-CoV under said conditions.